

GenCore version 5.1.3
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OW nucleic - nucleic search, using sw model

Run on: March 29, 2003, 20:49:12 ; Search time 330.604 Seconds

(without alignments)
8229.920 Million cell updates/sec

Title: US-09-988-971-1_COPY_517_684

Perfect score: 168

Sequence: 1 gccacacgcg9ccctg9.....gcctccacgtgccaagtc 168

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthm:*
3: em_estlm:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlm:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtc:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	168	100.0	778 12	BG178487 602328305
2	168	100.0	877 9	AL541041 AL541041
3	168	100.0	986 14	BQ054265 AGENCOURT
4	168	100.0	1002 14	BQ054265 AGENCOURT
5	168	100.0	1020 14	BQ054281 AGENCOURT
6	168	100.0	1069 14	BQ054281 AGENCOURT

7	161.6	96.2	878	14	BQ053486	BQ053486 AGENCOURT
8	124.8	74.3	627	10	B619854	B619854 AGENCOURT
9	124.8	74.3	640	14	BQ053006	BQ053006 H4019E02-
10	124.8	74.3	660	10	B6635615	B6635615 B6635615
11	123.8	73.7	670	9	A1510095	A1510095 mj43C04.y
12	114.4	68.1	377	9	AA959151	AA959151 vz51906.r
13	111	66.1	926	11	AK020837	AK020837 Mus muscu
14	90.8	54.0	506	17	B45150	B45150 HS-1060-B1-
15	83	49.4	541	13	B1898989	B1898989 480839 MA
16	67.2	40.0	389	10	BE015229	BE015229 127457 MA
17	52.4	31.2	525	13	B1348152	B1348152 da125c05.
18	50.4	30.0	507	9	AA051252	AA051252 mj43C04.r
19	43.6	26.0	527	10	AA669655	AA669655 hd32d07.x
20	43.6	26.0	546	10	BE397325	BE397325 601288664
21	43.6	26.0	559	10	AA668483	AA668483 EST380559
22	43.6	26.0	582	10	AA668724	AA668724 hd37a06.x
23	43.6	26.0	653	12	EC389203	EC389203 602413834
24	43.6	26.0	689	10	AM303654	AM303654 xv21n02.x
25	43.6	26.0	698	12	BE890610	BE890610 601431488
26	43.6	26.0	716	10	BE676457	BE676457 7130C12.x
27	43.6	26.0	720	10	AM188088	AM188088 xj92C01.x
28	43.6	26.0	751	12	BF448700	BF448700 7n33C09.x
29	43.6	26.0	789	9	AU134909	AU134909 AU134909
30	43.6	26.0	847	14	B0882902	B0882902 AGENCOURT
31	43.6	26.0	953	14	BQ642677	BQ642677 AGENCOURT
32	43.6	26.0	963	14	BQ659644	BQ659644 AGENCOURT
33	43.6	26.0	1003	14	BQ062356	BQ062356 AGENCOURT
34	43.6	26.0	1006	14	BQ058222	BQ058222 AGENCOURT
35	43.6	26.0	1047	14	BQ066753	BQ066753 AGENCOURT
36	43.6	26.0	1051	14	BQ063502	BQ063502 AGENCOURT
37	43.6	26.0	1070	14	BM909567	BM909567 AGENCOURT
38	42.6	25.4	708	10	BE675166	BE675166 7f03f06.x
39	42	25.0	619	9	A1572989	A1572989 tns64b01.x
40	41.6	24.8	340	10	AA481551	AA481551 36629 MAR
41	40.6	24.2	730	12	BG756039	BG756039 602716593
42	40.4	24.0	424	14	BQ305148	BQ305148 MR0-BT250
43	40	23.8	679	13	B1151721	B1151721 602915935
44	40	23.8	767	14	BM944156	BM944156 UI-M-BH0P
45	40	23.8	983	10	BB609447	BB609447 BB609447

ALIGNMENTS

RESULT 1
LOCUS BG178487 778 bp mRNA EST 06-FEB-2001
DEFINITION 602328305F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4429896 5',
ACCESSION BG178487
VERSION BG178487.1 GI:12685190
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM0182 row: 1 column: 01
High quality sequence atop: 657.
Location/Qualifiers 1..778

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4429896"
/clone_lib="NIH MGC 91"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMVSPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

BASE COUNT 179 a 224 c 230 g 145 t
ORIGIN

Query Match 100.0%; Score 168; DB 12; Length 778;
Best Local Similarity 100.0%; Pred. No. 6.3e-35;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTGGCCCTGGGCAAGTTTCCCGGCAAGTGGCCCGGCGAGCTGTCTGAGA 60
DB 463 GCCACAGCCGTGGCCCTGGGCAAGTTTCCCGGCAAGTGGCCCGGCGAGCTGTCTGAGA 522
QY 61 CTCGGGAGCCATTGACATCGTCTGAGATGAGACTGTGACGCTGTCTGAA 120
DB 523 CTCGGGAGCCATTGACATCGTCTGAGATGAGACTGTGACGCTGTCTGAA 582
QY 121 GTCTCAGCAGAGATATTAACATCCCGAGCTCCAGTGGCCAAAGTC 168
DB 583 GTCTCAGCAGAGATATTAACATCCCGAGCTCCAGTGGCCAAAGTC 630

RESULT 2
LOCUS ALS41041 877 bp mRNA linear EST 16-FEB-2001
DEFINITION ALS41041 LIT_FL002_PL1 Homo sapiens cDNA clone CS0DE005YK23 5 prime
, mRNA sequence.
ACCESSION ALS41041
VERSION ALS41041.1 GI:12871733
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 877)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
unpublished (2001)
JOURNAL Contact: Genoscope
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
Location/Qualifiers
1..877
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE005YK23"
/clone_lib="LIT_FL002_PL1"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
liang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 192 a 262 c 251 g 170 t 2 others
ORIGIN

Query Match 100.0%; Score 168; DB 9; Length 877;
Best Local Similarity 100.0%; Pred. No. 6.6e-35;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCACAGCCGTGGCCCTGGGCAAGTTTCCCGGCAAGTGGCCCGGCGAGCTGTCTGAGA 60
DB 469 GCCACAGCCGTGGCCCTGGGCAAGTTTCCCGGCAAGTGGCCCGGCGAGCTGTCTGAGA 548
QY 61 CTCGGGAGCCATTGACATCGTCTGAGATGAGACTGTGACGCTGTCTGAA 120
DB 549 CTCGGGAGCCATTGACATCGTCTGAGATGAGACTGTGACGCTGTCTGAA 608
QY 121 GTCTCAGCAGAGATATTAACATCCCGAGCTCCAGTGGCCAAAGTC 168
DB 609 GTCTCAGCAGAGATATTAACATCCCGAGCTCCAGTGGCCAAAGTC 656

RESULT 3
LOCUS B0054265 986 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT 6830248 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936339
5', mRNA sequence.
ACCESSION B0054265
VERSION B0054265.1 GI:19813605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 986)
NIH-MGC http://mgs.nci.nih.gov/.
NATIONAL INSTITUTE OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2125 row: 1 column: 12
High quality sequence step: 515.
Location/Qualifiers
1..986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5936339"
/clone_lib="NIH MGC 106"
/issue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

FEATURES
source
Location/Qualifiers
1..986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5936339"
/clone_lib="NIH MGC 106"
/issue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

BASE COUNT 211 a 291 c 276 g 207 t 1 others
ORIGIN

Query Match 100.0%; Score 168; DB 14; Length 986;
Best Local Similarity 100.0%; Pred. No. 6.9e-39;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTGGCCCTGGGCAAGTTTCCCGGCAAGTGGCCCGGCGAGCTGTCTGAGA 60
DB 381 GCCACAGCCGTGGCCCTGGGCAAGTTTCCCGGCAAGTGGCCCGGCGAGCTGTCTGAGA 440
QY 61 CTCGGGAGCCATTGACATCGTCTGAGATGAGACTGTGACGCTGTCTGAA 120
DB 441 CTCGGGAGCCATTGACATCGTCTGAGATGAGACTGTGACGCTGTCTGAA 500

QY 121 GTCTCAGCAGAGATTAACATCCCACTCCACGTCGCAAAATC 168
DB 501 GTCTCAGCAGAGATTAACATCCCACTCCACGTCGCAAAATC 548

RESULT 4
LOCUS B0052308
DEFINITION AGENCOURT_6868571 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933542
ACCESSION B0052308 1002 bp mRNA linear EST 29-MAR-2002
VERSION B0052308
KEYWORDS B0052308.1 GI:19811648
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1002)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM218 row: d column: 23
High quality sequence stop: 670.

FEATURES
source Location/Qualifiers
1..1002

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5933542"
/clone_1b="NIH MGC 106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC library."

BASE COUNT 221 a 296 c 288 g 197 t
ORIGIN

Query Match 100.0%; Score 168; DB 14; Length 1002;
Best Local Similarity 100.0%; Pred. No. 7e-39;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTCGTCGGGAGATTCCGGGAGGTGCGCCGCGACGTCGCTGAGA 60
DB 198 GCCACAGCCGTCGTCGGGAGATTCCGGGAGGTGCGCCGCGACGTCGCTGAGA 257
QY 61 CTCGGGAGCCATTGACCATGCTCTGAGAGTGAAGACTGCTGAGCGTCTGTGAA 120
DB 258 CTCGGGAGCCATTGACCATGCTCTGAGAGTGAAGACTGCTGAGCGTCTGTGAA 317
QY 121 GTCTCAGCAGAGATTAACATCCCACTCCACGTCGCAAAATC 168
DB 318 GTCTCAGCAGAGATTAACATCCCACTCCACGTCGCAAAATC 365

RESULT 5
LOCUS B0054281
DEFINITION AGENCOURT_6830234 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936362
5', mRNA sequence.

ACCESSION B0054281
VERSION B0054281.1 GI:19813621
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1020)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM215 row: j column: 11
High quality sequence stop: 556.

FEATURES
source Location/Qualifiers
1..1020

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5936362"
/clone_1b="NIH MGC 106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC library."

BASE COUNT 219 a 311 c 283 g 204 t 3 others
ORIGIN

Query Match 100.0%; Score 168; DB 14; Length 1020;
Best Local Similarity 100.0%; Pred. No. 7e-39;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTCGTCGGGAGATTCCGGGAGGTGCGCCGCGACGTCGCTGAGA 60
DB 314 GCCACAGCCGTCGTCGGGAGATTCCGGGAGGTGCGCCGCGACGTCGCTGAGA 373
QY 61 CTCGGGAGCCATTGACCATGCTCTGAGAGTGAAGACTGCTGAGCGTCTGTGAA 120
DB 374 CTCGGGAGCCATTGACCATGCTCTGAGAGTGAAGACTGCTGAGCGTCTGTGAA 433
QY 121 GTCTCAGCAGAGATTAACATCCCACTCCACGTCGCAAAATC 168
DB 434 GTCTCAGCAGAGATTAACATCCCACTCCACGTCGCAAAATC 481

RESULT 6
LOCUS B0052468
DEFINITION AGENCOURT_6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772
5', mRNA sequence.
ACCESSION B0052468
VERSION B0052468
KEYWORDS B0052468.1 GI:19811808
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1069)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

BASE COUNT	142 a	187 c	190 g	150 t	1 others
ORIGIN					

Query Match	68.1%;	Score 114.4;	DB 9;	Length 377;
Best Local Similarity	83.3%;	Pred. No. 2.5e-23;		
Matches 130; Conservative	0;	Mismatches 26;	Indels 0;	Gaps 0;

y 153 GAGTATTAACATCCCAGCGTCCACGTGGCCAAAGTC 168
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 125 GAGTACCAATGCCCAAGTGTATGTGGCTAAAGTC 160

RESULT 13					
AK020837					
LOCUS					
AK020837	926 bp	mRNA	linear	HTC 19-JAN-2007	
DEFINITION	Mus musculus adult retina cDNA, RIKEN full-length enriched library				

ACCESSION	AK020837
VERSION	AK020837.1
GI	12861542

SOURCE	Mus musculus (strain 129/SvEv) clone 11b:RIKEN
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100	100

ORGANISM
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
Rodentia; Sciurognathi;
Muridae; Murinae; Mus

REFERENCE
1. Carninci, P. and Hayashizaki, Y.
AUTHORS
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 15-44 (1999)
WORDS

MEDLINE
 PUBMED
 REFERENCE

TITLE	JOURNAL	YEAR	PAGES	DOI	PMID
Normalization and subtraction of capillary electrophoresis-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res.	10	(10)	1617-1630	(2000)
					20495374
					11042159
REFERENCE					
3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				

TITLE	JOURNAL	PUBLISHED
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res. 10 (11), 1757-1771 (2000)	20530913
		11076861
REFERENCES		
AUTHORS		
Kawai, J., Shinsagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komio, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakata, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.		

u

/clone_lib="CIT Human Genomic Sperm Library C"

/sex="M"

/note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in E-Coli DH10B"

BASE COUNT

105 a 128 c 161 g 112 t

ORIGIN

Query Match

Best Local Similarity 93.1%; Score 90.8; DB 17; Length 506;
Matches 95; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1

GCCACAGCCGTCGCTGGGAGATTTCCCGGAGGTGCCCCGCGAGCTGTGCTGAGA 60

Db 223

GCCACAGCCGTCGCTGGGAGATTTCCCGGAGGTGCCCCGCGAGCTGTGCTGAGA 282

Qy 61

CTGGGGAGACCATTCACATCGTCTGAGAGATGAGACTGG 102

Db 283

CTGGGGAGACCATTCACATCGTCTGAGAGATGAGACTGG 324

RESULT 15

BI898999

LOCUS

480839 MARC 2BOV Bos taurus cDNA 5', mRNA sequence. EST 16-OCT-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT

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Search completed: March 30, 2003, 02:49:21
Job time : 334.604 secs

Qy 1

GCCACAGCCGTCGCTGGGAGATTTCCCGGAGGTGCCCCGCGAGCTGTGCTGAGA 60

Db 435

GCCACAGCCGTCGCTGGGAGATTTCCCGGAGGTGCCCCGCGAGCTGTGCTGAGA 494

Qy 61

CTGGGGAGACCATTCACATCGTCTGAGAGATGAGACTGG 107

Db 495

CTGGGGAGACCATTCACATCGTCTGAGAGATGAGACTGG 541

FEATURES

source

1..541

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2BOV"

/issue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from testis, thymus,

semitendinosus muscle, longissimus muscle, pancreas,

adrenal, and endometrium."

BASE COUNT

120 a 157 g 104 t

ORIGIN

Query Match 49.4%; Score 83; DB 13; Length 541;
Best Local Similarity 86.0%; Pred. No. 4.8e-14;
Matches 92; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

